

SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company  
<120> Plant Lecithin:Cholesterol Acyltransferases  
<130> BB1262  
  
<140>  
<141>  
  
<150> 60/110,782  
<151> 1998-December-03  
  
<160> 14  
  
<170> Microsoft Office 97  
  
<210> 1  
<211> 542  
<212> DNA  
<213> Zea mays  
  
<220>  
<221> unsure  
<222> (433)  
  
<220>  
<221> unsure  
<222> (445)  
  
<220>  
<221> unsure  
<222> (472)  
  
<220>  
<221> unsure  
<222> (482)  
  
<220>  
<221> unsure  
<222> (495)  
  
<220>  
<221> unsure  
<222> (508)  
  
<220>  
<221> unsure  
<222> (513)  
  
<220>  
<221> unsure  
<222> (535)  
  
<400> 1  
gtggcgacaca gctacggcg caccgttcc tactgcggcg gcccttgccg 60  
tggcgcaagc gcttcgtccg gcgggttcgtg ccgcgttgcgg caccgtgggg aggcgtcgtc 120  
cttggcatgc tgacaatcgt cgccggcaac'aatctcggcc tgccgttcgt cgacccgctg 180  
gcgcgtcaagg gcgagtacctc gagcactcgtc ggccgtcgcc caaccccaac 240

gcatttagag ccgggcagcc actggtgacc acacggagca ggacgtacac ggcccacgac 300  
atggcgact tcctcgacgc catcggcta ggcggccaa ttgtgccgta ccagtcccg 360  
gtgctcccc tttccggga gtcgcata cgcgggtgc ccgtggctt tgccgtccg 420  
gggttggct gncacccg ggaanatgct gcctaacc gggaaagacga anttcgacgt 480  
gnacgcccatt gatnggcaa tgggaanac gngaacggg ctgggtcaaa cctgntgaac 540  
ct 542

<210> 2  
<211> 143  
<212> PRT  
<213> Zea mays

<400> 2  
Val Ala His Ser Tyr Gly Gly Thr Leu Ala His Gln Phe Leu Leu Arg  
1 5 10 15

Arg Pro Leu Pro Trp Arg Arg Arg Phe Val Arg Arg Phe Val Pro Val  
20 25 30

Ala Ala Pro Trp Gly Gly Val Val Leu Gly Met Leu Thr Ile Val Ala  
35 40 45

Gly Asn Asn Leu Gly Leu Pro Phe Val Asp Pro Leu Ala Leu Lys Gly  
50 55 60

Glu Tyr Arg Ser Leu Gln Ser Ser Leu Trp Pro Leu Pro Asn Pro Asn  
65 70 75 80

Ala Phe Arg Ala Gly Gln Pro Leu Val Thr Thr Arg Ser Arg Thr Tyr  
85 90 95

Thr Ala His Asp Met Ala Asp Phe Leu Asp Ala Ile Gly Leu Gly Ala  
100 105 110

Ala Ile Val Pro Tyr Gln Ser Arg Val Leu Pro Leu Phe Arg Glu Leu  
115 120 125

Pro Ser Pro Arg Val Pro Val Ala Cys Val Arg Pro Gly Leu Gly  
130 135 140

<210> 3  
<211> 921  
<212> DNA  
<213> Zea mays

<220>  
<221> unsure  
<222> (884)

<400> 3  
cgcgttagaa gatcgagtga gaagttgcgc gtgtgaagcc atcacaccaa taaaagatcg 60  
agatcatcca tggctagtt tctacttcag cagctgctgt ctctgctgct gtcctgctg 120  
ccctctcctc ttctgtctccg ggagcatcta tcaggaaacc atgctgtcag cgccaacaac 180  
ttccacccca ttcttcttgtt agctgggtg agctgcagcg acctggaggc acgcctcacc 240  
gaggagtacc ggccgtcggt gcccactgc ggcgcctatga agggaaagggt gtggttcggt 300  
ctgttggaga acagttcgga gctgctgtct cgtgactacg tgcagtgcctt cgaggagcag 360  
atgagcctcg tctacgaccc tgccatcaac gagtaccggc acctcgccgg cgtcgagacg 420  
cgagtgcctca acttcggctc cacaagagcc tttagccaca agaaccctt caagtcagac 480  
tggtgcctcg gaaagctgag agccgcactg gaagacatgg gataccgaga cggagacacc 540  
atgttcggag cccctacga ctccgctac ggcggccgt ccccgccca gacgtccgag 600

gtgtactccc gctacttcaa ggagctgatg gagctggtcg aggccgcgag cgagaggacc 660  
cggaagaagg ccgtcatcct cggcacacgc ttcggcgcca tggtcgcgcgct cgagttcgtc 720  
cggaacactc cgcggcggtg gcggcgcgag cacatcgagc gcctcgctct ggtcgccg 780  
acgctccccg ggggttcct ggagccgtg cgcaacttcg cgtccggac ggacatcctc 840  
tacgtgccag cgacgacgcc gctggccacg cgagccatgt tgangagctt cgagaacgcc 900  
atcgtgaatt cccgtcgccg g 921

<210> 4  
<211> 233  
<212> PRT  
<213> Zea mays

<400> 4

Met Ala Ser Ser Leu Leu Gln Gln Leu Leu Ser Leu Leu Leu Leu Leu  
1 5 10 15

Leu Pro Ser Pro Leu Arg Leu Arg Glu His Leu Ser Gly Asn His Ala  
20 25 30

Val Ser Ala Asn Asn Phe His Pro Ile Phe Leu Val Ala Gly Val Ser  
35 40 45

Cys Ser Asp Leu Glu Ala Arg Leu Thr Glu Glu Tyr Arg Pro Ser Val  
50 55 60

Pro His Cys Gly Ala Met Lys Gly Lys Gly Trp Phe Gly Leu Trp Lys  
65 70 75 80

Asn Ser Ser Glu Leu Leu Ser Arg Asp Tyr Val Gln Cys Phe Glu Glu  
85 90 95

Gln Met Ser Leu Val Tyr Asp Pro Ala Ile Asn Glu Tyr Arg Asn Leu  
100 105 110

Ala Gly Val Glu Thr Arg Val Pro Asn Phe Gly Ser Thr Arg Ala Phe  
115 120 125

Ser His Lys Asn Pro Leu Lys Ser Asp Trp Cys Leu Gly Lys Leu Arg  
130 135 140

Ala Ala Leu Glu Asp Met Gly Tyr Arg Asp Gly Asp Thr Met Phe Gly  
145 150 155 160

Ala Pro Tyr Asp Phe Arg Tyr Ala Pro Pro Ser Pro Gly Gln Thr Ser  
165 170 175

Glu Val Tyr Ser Arg Tyr Phe Lys Glu Leu Met Glu Leu Val Glu Ala  
180 185 190

Ala Ser Glu Arg Thr Arg Lys Lys Ala Val Ile Leu Gly His Ser Phe  
195 200 205

Gly Gly Met Val Ala Leu Glu Phe Val Arg Asn Thr Pro Pro Ala Trp  
210 215 220

Arg Arg Glu His Ile Glu Arg Leu Val  
225 230

<210> 5  
<211> 1217

<212> DNA

<213> Glycine max

<400> 5

ctttcatctg cgaatcatgg taccctctca tcaagaaaaaa gaatggatgg ttccagactt 60  
ggtttatttc cagtgtcata cttgcctc tcaactcaatg ctggccgaa cgcatgaccc 120  
ttcattacca ccaagaactc gatgattact tcaacactcc tgggttgag acccggtcc 180  
ctcaacttgg ttccaccaac tctcttctt atctcaatcc tcgtctcaag catatcaccc 240  
gatacatggc acccctggta gattcattac aaaagcttgg ctacgcttat ggtgagactc 300  
tgtttggagc cccttatgac ttttagatatg gtcttagtgc tgaaggctac ccttcacaag 360  
tgggttccaa gttcctcaaa gatctaaaga atttgataga agaagcaagc aattccaata 420  
atgggaagcc agtgatactt ctctcccaca gtttaggagg cctatttgc ctacaactac 480  
taaatagaaa cccccctct tggcgaaaaa aattcatcaa acacttcat gctcttcag 540  
ctccatgggg tgggtgtata gacgaaatgt acaccttgc atctggcaac actttggag 600  
tgcccctagt ggaccctta ttagtgaggg atgaacaaag aagctccgag agtaaccctt 660  
ggctttgcc taacccaaaa attttggtc ctcaaaaaacc aatagtgata actccaatta 720  
ggccttattc agctcatgac atgggttatt ttctaaaaga cattgggttt cctgaagggg 780  
tttaccccta tgaaacacga attctaccct tgatagggaa cataaaagca ccacaagtgc 840  
ctataacttg tattatgggaa acgggagtgg gaaccttggaa aacattgtt tatggaaag 900  
gtgattttga tgaacggcca gaaatatcat atggggatgg tgatggaaacg gtgaacttgg 960  
tgagcttggg ggcgcttcaa tcactatggaa aagaggagaa aaatcaatac cttaaagtgg 1020  
ttaagataga tgggtgtct catacttcaa tacttaagga tgaagttgca ctaaatgaaa 1080  
tagtaggtga gattacttca attaatttctc atgctgagct cggtttaagt aatttgggttt 1140  
cggggtaat gatcagggtg tttgaacgac aattatagat tcgttgcctg caaattaaat 1200  
tttgtgtggg gagttga 1217

<210> 6

<211> 381

<212> PRT

<213> Glycine max

<400> 6

Phe Ile Cys Glu Ser Trp Tyr Pro Leu Ile Lys Lys Lys Asn Gly Trp  
1 5 10 15

Phe Arg Leu Trp Phe Asp Ser Ser Val Ile Leu Ala Pro Phe Thr Gln  
20 25 30

Cys Phe Ala Glu Arg Met Thr Leu His Tyr His Gln Glu Leu Asp Asp  
35 40 45

Tyr Phe Asn Thr Pro Gly Val Glu Thr Arg Val Pro His Phe Gly Ser  
50 55 60

Thr Asn Ser Leu Leu Tyr Leu Asn Pro Arg Leu Lys His Ile Thr Gly  
65 70 75 80

Tyr Met Ala Pro Leu Val Asp Ser Leu Gln Lys Leu Gly Tyr Ala Asp  
85 90 95

Gly Glu Thr Leu Phe Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala  
100 105 110

Ala Glu Gly His Pro Ser Gln Val Gly Ser Lys Phe Leu Lys Asp Leu  
115 120 125

Lys Asn Leu Ile Glu Glu Ala Ser Asn Ser Asn Asn Gly Lys Pro Val  
130 135 140

Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu Gln Leu Leu  
 145 150 155 160  
 Asn Arg Asn Pro Pro Ser Trp Arg Lys Lys Phe Ile Lys His Phe Ile  
 165 170 175  
 Ala Leu Ser Ala Pro Trp Gly Gly Ala Ile Asp Glu Met Tyr Thr Phe  
 180 185 190  
 Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val Asp Pro Leu Leu Val  
 195 200 205  
 Arg Asp Glu Gln Arg Ser Ser Glu Ser Asn Leu Trp Leu Leu Pro Asn  
 210 215 220  
 Pro Lys Ile Phe Gly Pro Gln Lys Pro Ile Val Ile Thr Pro Ile Arg  
 225 230 235 240  
 Pro Tyr Ser Ala His Asp Met Val Asp Phe Leu Lys Asp Ile Gly Phe  
 245 250 255  
 Pro Glu Gly Val Tyr Pro Tyr Glu Thr Arg Ile Leu Pro Leu Ile Gly  
 260 265 270  
 Asn Ile Lys Ala Pro Gln Val Pro Ile Thr Cys Ile Met Gly Thr Gly  
 275 280 285  
 Val Gly Thr Leu Glu Thr Leu Phe Tyr Gly Lys Gly Asp Phe Asp Glu  
 290 295 300  
 Arg Pro Glu Ile Ser Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Val  
 305 310 315 320  
 Ser Leu Leu Ala Leu Gln Ser Leu Trp Lys Glu Glu Lys Asn Gln Tyr  
 325 330 335  
 Leu Lys Val Val Lys Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys  
 340 345 350  
 Asp Glu Val Ala Leu Asn Glu Ile Val Gly Glu Ile Thr Ser Ile Asn  
 355 360 365  
 Ser His Ala Glu Leu Gly Leu Ser Asn Leu Phe Ser Gly  
 370 375 380  
 <210> 7  
 <211> 1440  
 <212> DNA  
 <213> Zea mays  
 <400> 7  
 gcacgagccg acaacatcat ggcgaggatt ccccaggttc tggcgccgt cctcctcctg 60  
 ctgctccccg ccgtctccg ggagctgatg atcgaccgcg ggccctgccc gaagcgctgc 120  
 cggcgccagg tcctcctcca cccgctggtg ctgggtgccc ggctgacgtg cagcgagctg 180  
 gacgcgcggc tcacggacgc ctaccggccc ttccgcgcgg cgtgcgtatga aggggaagg 240  
 ctggttcgcc tctggaccaa ctgctccgac ctgcccgcgc accactacgt gcggtgcttc 300  
 atggagcaga tggccctcgat ctacgacccc gtcgcgaacg actaccggaa cctgccccggc 360  
 gtcgagacgc gctgtgcgcaaa ttccggctcc tcccgaggat tccagaagaa cccggagcac 420  
 acgaccttgtt cctggtgctt cgaggtcctc agaaaacgagc tggcaaggcc cgggttaccgc 480  
 gacggcgaca ccctgttcgg ggccccgtac gacctccgct acggcccgcc ggtgccccggc 540

cagccatcga ggtcttctcc ggctacttcc gtcggctggc cgaggcctcggt cgaggacgcg 600  
 agccgaaga accggggcaag gaagggtgate ctcttcggc acagcttcgg gggcatggtg 660  
 gcgctggagt tcgtccggag cactccatg gcggtggcgag acaggtacat caagcaccc 720  
 ttccctcgctcg cccccgggtgcc ggcggaaaggg ttcgtgaagc cgctgcagta cttcgtctcc 780  
 gggtccaacc tgatgtacgt cccgacagtc agctcgctcg agcctgcctt taggcccgtg 840  
 tggcggacct tcgagtcctc cctcgtaac ttcccctccc cagcgggttt cgggcgcagg 900  
 ccgctcgctgg tcaccgcgcg gaggaactac tccgcctacg acctggagga ctcctcgctc 960  
 gccgtcggtct acggcgccgg cgtggagccc ttcaggagac gggccgtccc caagatgagc 1020  
 tacttccagg ccccaatggt gccgaccacg tgcataaca ggggtgggcaa cgacacgccc 1080  
 gaggcagtcg tctactggg cggcgaactc gacgcgaccc cggagatagt gtacggcgc 1140  
 ggggacaattt ccatcaattt ggtcagcatg ctggcggttcg acgagaagat gcgcggcag 1200  
 ccggaacaga acaagggtta caagtcgatc aagattcgtg gggcccagca cggtactatt 1260  
 gtgacagacg acacggcgct caagcgggtc atgcacgaaa tccttgaagc gaatcgtagt 1320  
 taggctactc acaatgggaa tttcatgtct ctgtttccaa aaatgccaca tcagatttat 1380  
 ggtgaatga aataccctct ctcaatagag agtttcatct caaaaaaaaaaaaaaa 1440

<210> 8  
 <211> 434  
 <212> PRT  
 <213> Zea mays

<400> 8

Met Ala Arg Ile Pro Gln Val Leu Ala Pro Leu Leu Leu Leu Leu Leu  
 1 5 10 15

Pro Ala Gly Leu Arg Glu Leu Met Ile Asp Arg Arg Pro Leu Pro Lys  
 20 25 30

Arg Cys Arg Arg Glu Val Leu Leu His Pro Leu Val Leu Val Pro Gly  
 35 40 45

Leu Thr Cys Ser Glu Leu Asp Ala Arg Leu Thr Asp Ala Tyr Arg Pro  
 50 55 60

Phe Arg Ala Ala Cys Asp Glu Gly Glu Gly Leu Val Arg Leu Trp Thr  
 65 70 75 80

Asn Cys Ser Asp Leu Pro Ala His His Tyr Val Arg Cys Phe Met Glu  
 85 90 95

Gln Met Ala Leu Val Tyr Asp Pro Val Ala Asn Asp Tyr Arg Asn Leu  
 100 105 110

Pro Gly Val Glu Thr Arg Val Arg Asn Phe Gly Ser Ser Arg Gly Phe  
 115 120 125

Gln Lys Asn Pro Glu His Thr Thr Trp Ser Trp Cys Phe Glu Val Leu  
 130 135 140

Arg Asn Glu Leu Ala Arg Ala Gly Tyr Arg Asp Gly Asp Thr Leu Phe  
 145 150 155 160

Gly Ala Pro Tyr Asp Leu Arg Tyr Ala Pro Pro Val Pro Gly Gln Pro  
 165 170 175

Ser Arg Ser Ser Pro Ala Thr Ser Val Gly Trp Pro Ser Leu Val Glu  
 180 185 190

Asp Ala Ser Arg Lys Asn Arg Gly Arg Lys Val Ile Leu Phe Gly His  
 195 200 205

Ser Phe Gly Gly Met Val Ala Leu Glu Phe Val Arg Ser Thr Pro Met  
 210 215 220  
 Ala Trp Arg Asp Arg Tyr Ile Lys His Leu Phe Leu Val Ala Pro Val  
 225 230 235 240  
 Pro Ala Glu Gly Phe Val Lys Pro Leu Gln Tyr Phe Val Ser Gly Ser  
 245 250 255  
 Asn Leu Met Tyr Val Pro Thr Val Ser Ser Leu Glu Pro Ala Phe Arg  
 260 265 270  
 Pro Met Trp Arg Thr Phe Glu Ser Ser Leu Val Asn Phe Pro Ser Pro  
 275 280 285  
 Ala Val Phe Gly Arg Arg Pro Leu Val Val Thr Ala Arg Arg Asn Tyr  
 290 295 300  
 Ser Ala Tyr Asp Leu Glu Asp Leu Leu Val Ala Val Gly Tyr Gly Ala  
 305 310 315 320  
 Gly Val Glu Pro Phe Arg Arg Arg Ala Val Pro Lys Met Ser Tyr Phe  
 325 330 335  
 Gln Ala Pro Met Val Pro Thr Thr Cys Met Asn Gly Val Gly Asn Asp  
 340 345 350  
 Thr Pro Glu Gln Leu Val Tyr Trp Asp Gly Asp Phe Asp Ala Thr Pro  
 355 360 365  
 Glu Ile Val Tyr Gly Asp Gly Asp Asn Ser Ile Asn Leu Val Ser Met  
 370 375 380  
 Leu Ala Phe Asp Glu Lys Met Arg Arg Gln Pro Glu Gln Asn Lys Val  
 385 390 395 400  
 Tyr Lys Ser Ile Lys Ile Arg Gly Ala Gln His Gly Thr Ile Val Thr  
 405 410 415  
 Asp Asp Thr Ala Leu Lys Arg Val Met His Glu Ile Leu Glu Ala Asn  
 420 425 430  
 Arg Ser

<210> 9  
 <211> 1500  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> unsure  
 <222> (536)

<400> 9  
 ggccacagta gcccgggtt gcgatggtcc acgatatggc ttcttgttcc cgtggcgca 60  
 cgatcggtct gtccaaattt gcgagcacga cggaggcgcc accgaagcag ctggccccc 120  
 tggtggttgtt gcccgggtac gccaccaacg agctcgacgc ggccttcacg gagctgtacc 180  
 acccgtcgta accgcgtc accgcacaagg ggaaaggctg gttccgcctc tacctaact 240

acacggcgct ggaggacgcc gccgacgtgc gctgyttcgc cgagcagatg gccacggcgt 300  
 acgacgcggc gtccgacgac taccgaacg cccaggcggt ggagacccgc gtcccttct 360  
 tcggatccac ccgggccttc cgctaccccg acccagaccc gagaacttc tcgtacatgg 420  
 acaagttcgt gtcgcggctg gagcggtcg ctgaccgcga cggcgagaac ctgttcggc 480  
 cggcctacga ctcccggtac gccgtcgcgc cggcaggcca cccgtcgagg gtcgcngacg 540  
 ccttcttcgg gcgcctcagg aggctgttag agagggcgag cgggctaacc ggaggaggc 600  
 cggtgaccat cggtggcgac agctacggcg gcacgggtggc gcaccagtgc ctactgcggc 660  
 ggccttgcg gtggcgagg cgcttcgtcc ggccgggtcg gcccgttgcc gcccgtggg 720  
 gaggcgctgt cttggcatg ctgacaatcg tccggcggcaa caatctcgcc ctgcccgtcg 780  
 tcgaccccgct ggcgctcaag ggcgagtagc ggagcctgca gagcagcctc tggccgtcg 840  
 ccaacccaa cgcattaga gccgggcage cactgggtac cacacggagc aggacgtaca 900  
 cggccccacga catggcgac ttcttcgacg ccacgggtcg aggccggca attgtgcgt 960  
 accagtcggc cgtgtcgccc ctgttccggg agctgcccattc tccgggggtg cccgtggctt 1020  
 gtgtcgctgg ggtgggtcg gacacggcg agatgctggc ctacccggga gacgactcg 1080  
 acgtgacgcc gatgatggc atgggagacg gogacgggtcg ggtcaacctg gtgagcctcc 1140  
 tcgctgtcga ccctgcgtgg aggcttcata cagttactt taggatgctc aaggtgcgca 1200  
 acgtgtcaca cacgggcctc ttctggacg atgctgtctc cggcgttatac attagcggca 1260  
 tcctacggcc caattaataa ttcaactcaga catccgtacg tgcaaaaactg ttccggaaact 1320  
 tcacgaaaaag tttagataac aaatttcat cgttagcattt taaggaaata ggtggtaagc 1380  
 tctaaatttt acattattttt ttccgattaa gggctaaaca tgaggatgt acctcctgtat 1440  
 ggtactcttt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

<210> 10  
 <211> 417  
 <212> PRT  
 <213> Zea mays

<400> 10  
 Met Val His Asp Met Ala Ser Cys Ser Arg Gly Gly Thr Ile Val Leu  
 1 5 10 15

Ser	Lys	Phe	Ala	Ser	Thr	Thr	Arg	Arg	Ala	Pro	Lys	Gln	Leu	Pro	Pro
20							25						30		

Val	Val	Val	Val	Pro	Gly	Tyr	Ala	Thr	Asn	Glu	Leu	Asp	Ala	Arg	Leu
35						40							45		

Thr	Glu	Leu	Tyr	His	Pro	Ser	Ser	Pro	Arg	Cys	Ala	His	Lys	Gly	Lys
50						55					60				

Gly	Trp	Phe	Arg	Leu	Tyr	Leu	Asn	Tyr	Thr	Ala	Leu	Glu	Asp	Ala	Ala
65						70					75			80	

Asp	Val	Arg	Cys	Phe	Ala	Glu	Gln	Met	Ala	Thr	Ala	Tyr	Asp	Ala	Ala
85								90					95		

Ser	Asp	Asp	Tyr	Arg	Asn	Ala	Gln	Gly	Val	Glu	Thr	Arg	Val	Pro	Phe
100								105					110		

Phe	Gly	Ser	Thr	Arg	Ala	Phe	Arg	Tyr	Pro	Asp	Pro	Asp	Arg	Arg	Asn
115							120					125			

Phe	Ser	Tyr	Met	Asp	Lys	Phe	Val	Ser	Arg	Leu	Glu	Arg	Leu	Ala	Tyr
130								135			140				

Arg	Asp	Gly	Glu	Asn	Leu	Phe	Gly	Ala	Pro	Tyr	Asp	Phe	Arg	Tyr	Ala
145						150				155			160		

Val	Ala	Pro	Pro	Gly	His	Pro	Ser	Arg	Val	Ala	Asp	Ala	Phe	Phe	Gly
165									170			175			

Arg Leu Arg Arg Leu Val Glu Arg Ala Ser Arg Ala Asn Gly Gly Gly  
 180 185 190  
 Pro Val Thr Ile Val Ala His Ser Tyr Gly Gly Thr Val Ala His Gln  
 195 200 205  
 Phe Leu Leu Arg Arg Pro Leu Pro Trp Arg Arg Arg Phe Val Arg Arg  
 210 215 220  
 Phe Val Pro Val Ala Ala Pro Trp Gly Gly Val Val Leu Gly Met Leu  
 225 230 235 240  
 Thr Ile Val Ala Gly Asn Asn Leu Gly Leu Pro Phe Val Asp Pro Leu  
 245 250 255  
 Ala Leu Lys Gly Glu Tyr Arg Ser Leu Gln Ser Ser Leu Trp Pro Leu  
 260 265 270  
 Pro Asn Pro Asn Ala Phe Arg Ala Gly Gln Pro Leu Val Thr Thr Arg  
 275 280 285  
 Ser Arg Thr Tyr Thr Ala His Asp Met Ala Asp Phe Leu Asp Ala Ile  
 290 295 300  
 Gly Leu Gly Ala Ala Ile Val Pro Tyr Gln Ser Arg Val Leu Pro Leu  
 305 310 315 320  
 Phe Arg Glu Leu Pro Ser Pro Arg Val Pro Val Ala Cys Val Val Gly  
 325 330 335  
 Val Gly Leu Asp Thr Pro Glu Met Leu Ala Tyr Pro Gly Asp Asp Phe  
 340 345 350  
 Asp Val Thr Pro Met Met Val Met Gly Asp Gly Asp Gly Leu Val Asn  
 355 360 365  
 Leu Val Ser Leu Leu Ala Val Asp Pro Ala Trp Arg Leu Pro Thr Ala  
 370 375 380  
 Tyr Phe Arg Met Leu Lys Val Arg Asn Val Ser His Thr Gly Leu Phe  
 385 390 395 400  
 Val Asp Asp Ala Ala Leu Ala Val Ile Ile Ser Ala Ile Leu Arg Pro  
 405 410 415

#### Asn

```

<210> 11
<211> 1660
<212> DNA
<213> Zea mays

<400> 11
gcacgagcgc agtagaagat cgagtggagaa gttgcgcgtg tgaagccatc acaccaatta 60
aagatcgaga tcatccatgg cttagttctt acttcagcag ctgctgtctc tgctgctgct 120
cctgctgccc tctcccttcc gtctccggga gcaatctatca ggaaaccatg ctgtcagcgc 180
caacaacttc cacccatct ttctggtagc tggggtgagc tgcagcggacc tggaggcagc 240
cctcaccgag gaggatccggc cgtcggtgcc gcactgcggc gccatgaagg ggaagggtg 300

```

gttcggctcg	tggagaaca	gttcggagct	gctgtctcg	gactacgtgc	agtgc	ttcga	360	
ggagcagatg	agcctcg	tct	acgacc	cgtgc	catca	aac	tgccggcgt	420
cgagacgcga	gtgccc	aact	tcgg	ctccac	aagag	cccttc	agccacaaga	480
gtcagactgg	tgc	cctcg	gaa	agctg	agagc	gcactggaa	gacatggat	540
agacaccatg	ttcgg	gagccc	cctac	gactt	ccgct	acgcg	ccgccc	600
gtccgagg	gtg	acttccc	gct	acttca	agg	gatgg	gttgc	660
gaggacc	gg	ccg	gg	gg	cc	gg	ccg	720
gttcgtcc	gg	aa	act	ccgc	cc	gg	ccgc	780
cgccgc	ac	act	ccgc	gg	gg	gtc	ccgt	840
ctccccgg	cg	tt	cc	ctt	gg	gc	ccgt	900
catcct	ta	c	tc	tc	gg	gt	gttgc	960
gtgc	ca	g	cc	cc	cc	gg	gg	1020
ggtc	acc	agg	cc	cc	cc	gg	gg	1080
cg	c	gg	cc	cc	cc	gg	gg	1140
cttc	cg	gg	cc	cc	cc	gg	gg	1200
gccc	gt	gg	cc	cc	cc	gg	gg	1260
gg	at	tt	cc	cc	cc	gg	gg	1320
cg	tc	cc	cc	cc	cc	gg	gg	1380
tttc	cg	gg	cc	cc	cc	gg	gg	1440
gccc	gt	gg	cc	cc	cc	gg	gg	1500
gttattt	tt	tt	tt	tt	tt	tt	tt	1560
ttat	tt	tt	tt	tt	tt	tt	tt	1620
ttat	tt	tt	tt	tt	tt	tt	tt	1660
atagtagc	ag	ta	ca	aa	ac	aa	aa	
at	at	aa	aa	aa	aa	aa	aa	

<210> 12  
<211> 439  
<212> PRT  
<213> Zea mays

<400> 12

Met Ala Ser Ser Leu Leu Gln Gln Leu Leu Ser Leu Leu Leu Leu  
1 5 10 15

Leu Pro Ser Pro Leu Arg Leu Arg Glu His Leu Ser Gly Asn His Ala  
20 25 30

Val Ser Ala Asn Asn Phe His Pro Ile Phe Leu Val Ala Gly Val Ser  
35 40 45

Cys Ser Asp Leu Glu Ala Arg Leu Thr Glu Glu Tyr Arg Pro Ser Val  
50 55 60

Pro His Cys Gly Ala Met Lys Gly Lys Gly Trp Phe Gly Leu Trp Lys  
65 70 75 80

Asn Ser Ser Glu Leu Leu Ser Arg Asp Tyr Val Gln Cys Phe Glu Glu  
85 90 95

Gln Met Ser Leu Val Tyr Asp Pro Ala Ile Asn Glu Tyr Arg Asn Leu  
100 105 110

Ala Gly Val Glu Thr Arg Val Pro Asn Phe Gly Ser Thr Arg Ala Phe  
115 120 125

Ser His Lys Asn Pro Leu Lys Ser Asp Trp Cys Leu Gly Lys Leu Arg  
130 135 140

Ala Ala Leu Glu Asp Met Gly Tyr Arg Asp Gly Asp Thr Met Phe Gly  
145 150 155 160

Ala Pro Tyr Asp Phe Arg Tyr Ala Pro Pro Ser Pro Gly Gln Thr Ser  
 165 170 175  
 Glu Val Tyr Ser Arg Tyr Phe Lys Glu Leu Met Glu Leu Val Glu Ala  
 180 185 190  
 Ala Ser Glu Arg Thr Arg Lys Lys Ala Val Ile Leu Gly His Ser Phe  
 195 200 205  
 Gly Gly Met Val Ala Leu Glu Phe Val Arg Asn Thr Pro Pro Ala Trp  
 210 215 220  
 Arg Arg Glu His Ile Glu Arg Leu Val Leu Val Ala Pro Thr Leu Pro  
 225 230 235 240  
 Gly Gly Phe Leu Glu Pro Val Arg Asn Phe Ala Ser Gly Thr Asp Ile  
 245 250 255  
 Leu Tyr Val Pro Ala Thr Thr Pro Leu Ala Thr Arg Ala Met Trp Arg  
 260 265 270  
 Ser Phe Glu Ser Ala Ile Val Asn Phe Pro Ser Pro Ala Val Phe Gly  
 275 280 285  
 Arg Leu Gln Ala Pro Leu Val Val Thr Arg Glu Arg Asn Tyr Ser Ala  
 290 295 300  
 Ser Ala His Asp Met Glu Arg Phe Leu Ala Ala Val Gly Ser Gly Glu  
 305 310 315 320  
 Ala Ala Glu Pro Phe Arg Arg Ala Val Pro Lys Met Gly Ser Phe  
 325 330 335  
 Ala Ala Pro Met Val Pro Met Thr Tyr Ile Ser Gly Val Gly Asn Arg  
 340 345 350  
 Thr Pro Leu Arg Leu Val Phe Trp Gly Glu Asp Phe Asp Ala Ala Pro  
 355 360 365  
 Glu Val Ala Ala Tyr Gly Asp Arg Asp Gly Lys Ile Asn Leu Ile Ser  
 370 375 380  
 Val Leu Ala Phe Glu Lys Glu Met Arg Arg Gln Pro Glu Gln Lys Lys  
 385 390 395 400  
 Gln Phe Lys Ser Ile Lys Ile Asn Lys Ala Gln His Ser Thr Ile Val  
 405 410 415  
 Thr Asp Asp Phe Ala Leu His Arg Val Ile Gln Glu Ile Val Glu Ala  
 420 425 430  
 Asn Asn Gln Lys Ile Pro Ser  
 435

<210> 13  
 <211> 1332  
 <212> DNA  
 <213> Glycine max

<400> 13

atgaagaagg aacaagaaga gggctcaag attgagggtt ctacactcac agttacagta	60
gttgttgcatt gctatgcaca tggggca gcaacctcgcccttgcatt	120
ctaataccag gtaacggagg gaaccaacta gaagcaaggt tgaccaatca gtacaagccc	180
tctactttca tctgcgaatc atggtaaccct ctcatacaaga aaaagaatgg atggttcaga	240
ctttggttt attccagtgt catacttgct ccttcactc aatgcttgc cgaacgcatg	300
acccttcatt accaccaaga actcgatgat tacttcaaca ctcctgggt tgagacccgg	360
gtccctcaact ttggttccac caactctt ctcatactca atcctcgatc caagcatatc	420
accggataca tggcacccct ggttagattca ttacaaaagc ttggctacgc tgatggtag	480
actctgttt gagcccccta tgactttaga tatggcttag ctgctgaagg tcacccttca	540
caagtgggtt ccaagttctt caaagatcta aagaatttg tagaagaagc aagcaattcc	600
aataatggga agccagtgtat acttctctcc cacagtttag gaggcctatt tgcctacaa	660
ctactaaata gaaacccccc ctcttgcgc aaaaaattca tcaaacadtt cattgctctt	720
tcagctccat ggggtggtgc tatagacgaa atgtacaccc ttgcatactgg caacacttg	780
ggagtgcggg tagtgaccc tttattagtg aggatgaac aaagaagctc cgagagtaac	840
ctttggctt tgcctaaacc aaaaattttt ggtcctcaaa aaccaatagt gataactcca	900
attaggcctt attcagctca tgacatgggt gattttctaa aagacattgg tttcctgaa	960
ggggtttatac cttatgaaac acgaattcta cccttgataa ggaacataaa agcaccacaa	1020
gtgcctataa cttgtattt gggAACGGGA tggggAACCT tggAAACATT gtttatggg	1080
aaaggtgatt ttgatgaacg gccagaaata tcatatgggg atggatgg aacggtaac	1140
ttggtgagct tggcgcgt tcaatcacta tggaaagagg agaaaaatca atacctaaa	1200
gtggtaaga tagatgggt gtctcataactt aagatgaagt tgcactaaat	1260
gaaatagtag gtgagattac ttcaatataat tctcatgctg agctcggttt aagtaatttg	1320
tttcggggt aa	1332

<210> 14

<211> 443

<212> PRT

<213> Glycine max

<400> 14

Met Lys Lys Glu Gln Glu Glu Gly Leu Lys Ile Glu Val Ala Thr Leu			
1	5	10	15

Thr Val Thr Val Val Val Met Leu Ser Leu Leu Cys Thr Cys Gly			
20	25	30	

Ala Ser Asn Leu Asp Pro Leu Ile Leu Ile Pro Gly Asn Gly Gly Asn			
35	40	45	

Gln Leu Glu Ala Arg Leu Thr Asn Gln Tyr Lys Pro Ser Thr Phe Ile			
50	55	60	

Cys Glu Ser Trp Tyr Pro Leu Ile Lys Lys Asn Gly Trp Phe Arg			
65	70	75	80

Leu Trp Phe Asp Ser Ser Val Ile Leu Ala Pro Phe Thr Gln Cys Phe			
85	90	95	

Ala Glu Arg Met Thr Leu His Tyr His Gln Glu Leu Asp Asp Tyr Phe			
100	105	110	

Asn Thr Pro Gly Val Glu Thr Arg Val Pro His Phe Gly Ser Thr Asn			
115	120	125	

Ser Leu Leu Tyr Leu Asn Pro Arg Leu Lys His Ile Thr Gly Tyr Met			
130	135	140	

Ala Pro Leu Val Asp Ser Leu Gln Lys Leu Gly Tyr Ala Asp Gly Glu			
145	150	155	160

Thr Leu Phe Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Glu  
 165 170 175  
 Gly His Pro Ser Gln Val Gly Ser Lys Phe Leu Lys Asp Leu Lys Asn  
 180 185 190  
 Leu Ile Glu Glu Ala Ser Asn Ser Asn Asn Gly Lys Pro Val Ile Leu  
 195 200 205  
 Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu Gln Leu Leu Asn Arg  
 210 215 220  
 Asn Pro Pro Ser Trp Arg Lys Lys Phe Ile Lys His Phe Ile Ala Leu  
 225 230 235 240  
 Ser Ala Pro Trp Gly Gly Ala Ile Asp Glu Met Tyr Thr Phe Ala Ser  
 245 250 255  
 Gly Asn Thr Leu Gly Val Pro Leu Val Asp Pro Leu Leu Val Arg Asp  
 260 265 270  
 Glu Gln Arg Ser Ser Glu Ser Asn Leu Trp Leu Leu Pro Asn Pro Lys  
 275 280 285  
 Ile Phe Gly Pro Gln Lys Pro Ile Val Ile Thr Pro Ile Arg Pro Tyr  
 290 295 300  
 Ser Ala His Asp Met Val Asp Phe Leu Lys Asp Ile Gly Phe Pro Glu  
 305 310 315 320  
 Gly Val Tyr Pro Tyr Glu Thr Arg Ile Leu Pro Leu Ile Gly Asn Ile  
 325 330 335  
 Lys Ala Pro Gln Val Pro Ile Thr Cys Ile Met Gly Thr Gly Val Gly  
 340 345 350  
 Thr Leu Glu Thr Leu Phe Tyr Gly Lys Gly Asp Phe Asp Glu Arg Pro  
 355 360 365  
 Glu Ile Ser Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Val Ser Leu  
 370 375 380  
 Leu Ala Leu Gln Ser Leu Trp Lys Glu Glu Lys Asn Gln Tyr Leu Lys  
 385 390 395 400  
 Val Val Lys Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu  
 405 410 415  
 Val Ala Leu Asn Glu Ile Val Gly Glu Ile Thr Ser Ile Asn Ser His  
 420 425 430  
 Ala Glu Leu Gly Leu Ser Asn Leu Phe Ser Gly  
 435 440  
 <210> 15  
 <211> 432  
 <212> PRT  
 <213> Arabidopsis thaliana

<400> 15  
 Met Lys Lys Ile Ser Ser His Tyr Ser Val Val Ile Ala Ile Leu Val  
 1 5 10 15  
 Val Val Thr Met Thr Ser Met Cys Gln Ala Val Gly Ser Asn Val Tyr  
 20 25 30  
 Pro Leu Ile Leu Val Pro Gly Asn Gly Gly Asn Gln Leu Glu Val Arg  
 35 40 45  
 Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val Trp Cys Ser Ser Trp Leu  
 50 55 60  
 Tyr Pro Ile His Lys Lys Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp  
 65 70 75 80  
 Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met  
 85 90 95  
 Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly  
 100 105 110  
 Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr  
 115 120 125  
 Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val  
 130 135 140  
 Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu  
 145 150 155 160  
 Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro  
 165 170 175  
 Ser Arg Val Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu  
 180 185 190  
 Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His  
 195 200 205  
 Ser Leu Gly Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro  
 210 215 220  
 Ser Trp Arg Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro  
 225 230 235 240  
 Trp Gly Gly Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr  
 245 250 255  
 Leu Gly Val Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg  
 260 265 270  
 Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His  
 275 280 285  
 Asp Arg Thr Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala  
 290 295 300  
 Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val  
 305 310 315 320

Val Pro Tyr Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr  
325 330 335

Pro Gly Val Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro  
340 345 350

Glu Val Leu Met Tyr Gly Lys Gly Phe Asp Lys Gln Pro Glu Ile  
355 360 365

Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala  
370 375 380

Leu Lys Val Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His  
385 390 395 400

Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln  
405 410 415

Ile Ser Ile Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu  
420 425 430